as 70
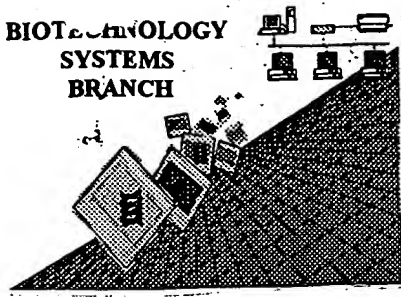0809

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/918,026_

Source: _OIPE_

Date Processed by STIC: _8/7/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/9₁8,026_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                         prevent "wrapping."

· 2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                  ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                        each n or Xaa can only represent a single residue. Please present the maximum number of each
                        residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                     Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                          (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                          This sequence is intentionally skipped

                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
                          <400> sequence id number
                          000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                            In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                       is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                      Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                      "Unknown." Please explain source of genetic material in <220> to <223> section.
                      (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                      listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n   n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent
                     any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 08/07/2001
PATENT APPLICATION: US/09/918,026   TIME: 13:57:45

Input Set : A:\isph-588.txt
Output Set: N:\CRF3\08072001\I918026.raw

Does Not Comply
Corrected Diskette Needed

```
    4 <110> APPLICANT: Rosanne M. Crooke
    5        Mark J. Graham
    6        Kristina M. Lemonidis
    9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COA CHOLESTEROL
ACYLTRANSFERASE-2 EXPRESSION
   11 <130> FILE REFERENCE: ISPH-0588
   13 <140> CURRENT APPLICATION NUMBER: US/09/918,026
   13 <141> CURRENT FILING DATE: 2001-07-30
   13 <160> NUMBER OF SEQ ID NOS: 65
```

ERRORED SEQUENCES

```
  987 <210> SEQ ID NO: 65
  988 <211> LENGTH: 20
  989 <212> TYPE: DNA
  990 <213> ORGANISM: Artificial Sequence
  992 <220> FEATURE:
  993 <223> OTHER INFORMATION: Antisense Oligonucleotide
  995 <400> SEQUENCE: 65
  996 ctaggtatgg caggaccaag                                          20
E--> 999  1
E--> 1002 18   delete - see next pages for more errors
```

```
199 <400> SEQUENCE: 5
200 cccgggcacc aagga                                              15
202 <210> SEQ ID NO: 6
203 <211> LENGTH: 25
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: PCR Probe
210 <400> SEQUENCE: 6
211 ctacgtgtat caggatgggc tgcgg                                   25
213 <210> SEQ ID NO: 7
214 <211> LENGTH: 19
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: PCR Primer
221 <400> SEQUENCE: 7
222 gaaggtgaag gtcggagtc                                          19
224 <210> SEQ ID NO: 8
225 <211> LENGTH: 20
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: PCR Primer
232 <400> SEQUENCE: 8
233 gaagatggtg atgggatttc                                         20
235 <210> SEQ ID NO: 9
236 <211> LENGTH: 20
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: PCR Probe
243 <400> SEQUENCE: 9
244 caagcttccc gttctcagcc                                         20
246 <210> SEQ ID NO: 10
247 <211> LENGTH: 1607
248 <212> TYPE: DNA
249 <213> ORGANISM: Mus musculus          see next page
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (30)...(1607)
255 <400> SEQUENCE: 10
256 ctgtgtgctg tccgctctac actggcacc atg cag cca aag gtg ccc cag ctt   53
257                                    Met Gln Pro Lys Val Pro Gln Leu
258                                     1               5
260 cgg agg aga gaa ggg ctg gga gag gag cag gag aag gga gcc cgt gga   101
261 Arg Arg Arg Glu Gly Leu Gly Glu Glu Gln Glu Lys Gly Ala Arg Gly
262      10              15                  20
264 gga gaa ggg aac gca agg aca cac gga acc cca gac ttg gtg caa tgg   149
```

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10042001\I918026.raw

```
    265 Gly Glu Gly Asn Ala Arg Thr His Gly Thr Pro Asp Leu Val Gln Trp
    266  25                      30              35                  40
W--> 268 act cga cat atg gag gct gtg aag acn cag ttt ctg gag caa gca cag    197
    269 Thr Arg His Met Glu Ala Val Lys Thr Gln Phe Leu Glu Gln Ala Gln
    270                          45              50                  55
    272 aga gag ttg gca gag ctg ttg gat cgg gcc cta tgg gag gct atg caa    245
    273 Arg Glu Leu Ala Glu Leu Leu Asp Arg Ala Leu Trp Glu Ala Met Gln
    274                  60              65                  70
    276 gct tac ccc aaa caa gac aga cct ctt ccc tcc gct gcc cca gat tct    293
    277 Ala Tyr Pro Lys Gln Asp Arg Pro Leu Pro Ser Ala Ala Pro Asp Ser
    278              75                  80                  85
    280 aca agc aag acc ccg gag tta cgc cct gga aaa cgg aaa gtt ttc gtc    341
    281 Thr Ser Lys Thr Pro Glu Leu Arg Pro Gly Lys Arg Lys Val Phe Val
    282          90                  95                 100
    284 gcc cgc aag tca ctg atc gat gag cta atg gag gtg caa cat ttc cga    389
    285 Ala Arg Lys Ser Leu Ile Asp Glu Leu Met Glu Val Gln His Phe Arg
    286 105                     110                 115                 120
    288 acc atc tac cac atg ttc ata gcg ggc cta tgg ttc ttg atc atc agc    437
    289 Thr Ile Tyr His Met Phe Ile Ala Gly Leu Trp Phe Leu Ile Ile Ser
    290                     125                 130                 135
    292 acc ctg gcc atc gac ttc att gat gag ggc agg ttg atg ctg gag ttt    485
    293 Thr Leu Ala Ile Asp Phe Ile Asp Glu Gly Arg Leu Met Leu Glu Phe
    294                 140                 145                 150
    296 gac tta ctc ctc ttc agc ttc gga cag ctg ccc ttg gcg ctg atg acc    533
    297 Asp Leu Leu Leu Phe Ser Phe Gly Gln Leu Pro Leu Ala Leu Met Thr
    298              155                 160                 165
    300 tgg gtt ccc atg ttc ctg tat acg ctc cta gtg ccc tac cag acc ctg    581
    301 Trp Val Pro Met Phe Leu Tyr Thr Leu Leu Val Pro Tyr Gln Thr Leu
    302          170                 175                 180
    304 tgg ctg tgg gcc agg ccg cgc gct ggg ggt gcc tgg atg ctg ggg gcc    629
    305 Trp Leu Trp Ala Arg Pro Arg Ala Gly Gly Ala Trp Met Leu Gly Ala
    306 185                     190                 195                 200
    308 agc ctg ggc tgc gtt ctg ctg gct gcc cac gct gtg gtg ctc tgc gtc    677
    309 Ser Leu Gly Cys Val Leu Leu Ala Ala His Ala Val Val Leu Cys Val
    310                     205                 210                 215
    312 ctg ccg gtg cac gtg tca gtg agg cat gag ctt ccg ccc gcc tcg cgc    725
    313 Leu Pro Val His Val Ser Val Arg His Glu Leu Pro Pro Ala Ser Arg
    314                     220                 225                 230
    316 tgc gtg ctg gtc ttt gag cag gtc aga ttg ctg atg aaa agc tac tcc    773
    317 Cys Val Leu Val Phe Glu Gln Val Arg Leu Leu Met Lys Ser Tyr Ser
    318                 235                 240                 245
    320 ttc ctg aga gag act gtg cct ggg atc ttt tgt gtc aga cga gga aag    821
    321 Phe Leu Arg Glu Thr Val Pro Gly Ile Phe Cys Val Arg Arg Gly Lys
    322         250                 255                 260
    324 ggc atc agc ccc cca agt ttc tcc agc tac ctc tac ttc ctc ttc tgc    869
    325 Gly Ile Ser Pro Pro Ser Phe Ser Ser Tyr Leu Tyr Phe Leu Phe Cys
    326 265                     270                 275                 280
    328 cct aca ctt atc tac aga gag aca tac ccc agg aca ccc agc atc agg    917
    329 Pro Thr Leu Ile Tyr Arg Glu Thr Tyr Pro Arg Thr Pro Ser Ile Arg
```

Input Set : **A:\isph-588.txt**
Output Set: **N:\CRF3\08072001\I918026.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:268 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:999 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:20 SEQ:65
M:254 Repeated in SeqNo=65